

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/170,042A

DATE: 03/16/2001  
TIME: 16:00:57

Input Set : D:\PF226D1.txt  
Output Set: N:\CRF3\03162001\I170042A.raw

3 <110> APPLICANT: Hastings, Gregg  
4 Dillon, Patrick  
6 <120> TITLE OF INVENTION: Human Neuronal Attachment Factor-1  
8 <130> FILE REFERENCE: PF226D1  
10 <140> CURRENT APPLICATION NUMBER: 09/170,042A  
C--> 11 <141> CURRENT FILING DATE: 1998-10-13  
13 <160> NUMBER OF SEQ ID NOS: 19  
15 <170> SOFTWARE: PatentIn version 3.0  
17 <210> SEQ ID NO: 1  
18 <211> LENGTH: 1105  
19 <212> TYPE: DNA  
20 <213> ORGANISM: homo sapiens  
22 <220> FEATURE:  
23 <221> NAME/KEY: CDS  
24 <222> LOCATION: (19)..(1011)  
26 <400> SEQUENCE: 1  
27 cgctgctcct gccgggtg atg gaa aac ccc agc ccg gcc gcc ctg gcc 51  
28 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly 10  
29 1 5  
31 aag gcc ctc tgc gct ctc ctc ctg gcc act ctc gcc gcc gcc ggc cag 99  
32 Lys Ala Leu Cys Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln 25  
33 15 20  
35 cct ctt ggg gga gag tcc atc tgt tcc gcc aga gcc ctg gcc aaa tac 147  
36 Pro Leu Gly Gly Glu Ser Ile Cys Ser Ala Arg Ala Leu Ala Lys Tyr 40  
37 30 35  
39 agc atc acc ttc acg ggc aag tgg agc cag acg gcc ttc ccc aag cag 195  
40 Ser Ile Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln 55  
41 45 50  
43 tac ccc ctg ttc cgc ccc cct gcc cag tgg tct tcg ctg ctg ggg gcc 243  
44 Tyr Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala 75  
45 60 65 70  
47 gcg cat agc tcc gac tac agc atg tgg agg aag aac cag tac gtc agt 291  
48 Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser 90  
49 80 85  
51 aac ggg ctg cgc gac ttt gcg gag cgc ggc gag gcc tgg gcg ctg atg 339  
52 Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met 105  
53 95 100  
55 aag gag atc gag gcg gcg ggg gag gcg ctg cag agc gtg cac gcg gtg 387  
56 Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val His Ala Val 120  
57 110 115  
59 ttt tcg gcg ccc gcc gtc ccc agc ggc acc ggg cag acg tcg gcg gag 435  
60 Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu 135  
61 125 130  
63 ctg gag gtg cag cgc agg cac tcg ctg gtc tcg ttt gtg gtg cgc atc 483  
64 Leu Glu Val Gln Arg Arg His Ser Leu Val Ser Phe Val Val Arg Ile 155  
65 140 145 150  
67 gtg ccc agc ccc gac tgg ttc gtg ggc gtg gac agc ctg gac ctg tgc 531

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```

68 Val Pro Ser Pro Asp Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys
69                               160                               165                               170
71 gac ggg gac cgt tgg cgg gaa cag gcg gcg ctg gac ctg tac ccc tac      579
72 Asp Gly Asp Arg Trp Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr
73                               175                               180                               185
75 gac gcc ggg acg gac agc ggc ttc acc ttc tcc tcc ccc aac ttc gcc      627
76 Asp Ala Gly Thr Asp Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala
77                               190                               195                               200
79 acc atc ccg cag gac acg gtg acc gag ata acg tcc tcc tct ccc agc      675
80 Thr Ile Pro Gln Asp Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser
81                               205                               210                               215
83 cac ccg gcc aac tcc ttc tac tac ccg cgg ctg aag gcc ctg cct ccc      723
84 His Pro Ala Asn Ser Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro
85 220                               225                               230                               235
87 atc gcc agg gtg aca ctg gtg cgg ctg cga cag agc ccc agg gcc ttc      771
88 Ile Ala Arg Val Thr Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe
89                               240                               245                               250
91 atc cct ccc gcc cca gtc ctg ccc agc agg gac aat gag att gta gac      819
92 Ile Pro Pro Ala Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp
93                               255                               260                               265
95 agc gcc tca gtt cca gaa acg ccg ctg gac tgc gag gtc tcc ctg tgg      867
96 Ser Ala Ser Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp
97                               270                               275                               280
99 tgc tcc tgg gga ctg tgc gga ggc cac tgt ggg agg ctc ggg acc aag      915
100 Ser Ser Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys
101                               285                               290                               295
103 agc agg act cgc tac gtc cgg gtc cag ccc gcc aac aac ggg agc ccc      963
104 Ser Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro
105 300                               305                               310                               315
107 tgc ccc gag ctc gaa gaa gag gct gag tgc gtc cct gat aac tgc gtc      1011
108 Cys Pro Glu Leu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val
109                               320                               325                               330
111 taagaccaga gccccgcagc ccctggggcc ccccgagacc atggggtgtc gggggctcct      1071
113 gtgcaggctc atgctgcagg cggccgaggg caca                               1105
116 <210> SEQ ID NO: 2
117 <211> LENGTH: 331
118 <212> TYPE: PRT
119 <213> ORGANISM: homo sapiens
121 <400> SEQUENCE: 2
123 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala
124 1                               5                               10                               15
127 Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu
128                               20                               25                               30
131 Ser Ile Cys Ser Ala Arg Ala Leu Ala Lys Tyr Ser Ile Thr Phe Thr
132                               35                               40                               45
135 Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg
136                               50                               55                               60
139 Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp
140 65                               70                               75                               80

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```

143 Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp
144      85      90      95
147 Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala
148      100      105      110
151 Ala Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala
152      115      120      125
155 Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg
156      130      135      140
159 Arg His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp
160 145      150      155      160
163 Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp
164      165      170      175
167 Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp
168      180      185      190
171 Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp
172      195      200      205
175 Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser
176      210      215      220
179 Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr
180 225      230      235      240
183 Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala Pro
184      245      250      255
187 Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro
188      260      265      270
191 Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu
192      275      280      285
195 Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr
196      290      295      300
199 Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu
200 305      310      315      320
203 Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val
204      325      330

```

207 &lt;210&gt; SEQ ID NO: 3

208 &lt;211&gt; LENGTH: 36

209 &lt;212&gt; TYPE: DNA

210 &lt;213&gt; ORGANISM: oligonucleotide

212 &lt;220&gt; FEATURE:

213 &lt;221&gt; NAME/KEY: primer\_bind

214 &lt;222&gt; LOCATION: (1)..(36)

215 &lt;223&gt; OTHER INFORMATION: 5' primer containing a BamHI restriction enzyme site followed by

216 21 nucleotides of NAD-1 coding sequence.

219 &lt;400&gt; SEQUENCE: 3

220 gccatacggg atccccagcc tcttggggga gagtcc

36

223 &lt;210&gt; SEQ ID NO: 4

224 &lt;211&gt; LENGTH: 35

225 &lt;212&gt; TYPE: DNA

226 &lt;213&gt; ORGANISM: oligonucleotide

228 &lt;220&gt; FEATURE:

229 &lt;221&gt; NAME/KEY: primer\_bind

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230 <222> LOCATION: (1)..(35)  
231 <223> OTHER INFORMATION: 3' primer containing complementary sequence to an XbaI site  
232 followed by 21 nucleotides of NAF-1 sequence.  
235 <400> SEQUENCE: 4 35  
236 ggcatacgtc tagattagac gcagttatca gggac  
239 <210> SEQ ID NO: 5  
240 <211> LENGTH: 41  
241 <212> TYPE: DNA  
242 <213> ORGANISM: oligonucleotide  
244 <220> FEATURE:  
245 <221> NAME/KEY: primer\_bind  
246 <222> LOCATION: (1)..(41).  
247 <223> OTHER INFORMATION: 5' primer containing a BamHI restriction enzyme site followed by  
248 8 nucleotides resembling an efficient signal for initiation of  
249 translation in eukaryotic cells followed by 21 nucleotides of  
250 NAF-1 sequence.  
253 <400> SEQUENCE: 5 41  
254 gccatacggg atccgccatc atggaaaacc ccagcccggc c  
257 <210> SEQ ID NO: 6  
258 <211> LENGTH: 35  
259 <212> TYPE: DNA  
260 <213> ORGANISM: oligonucleotide  
262 <220> FEATURE:  
263 <221> NAME/KEY: primer\_bind  
264 <222> LOCATION: (1)..(35)  
265 <223> OTHER INFORMATION: 3' primer containing the cleavage site for XbaI restriction  
266 endonuclease and 21 nucleotides complementary to the  
267 3' end of the translated sequence of the NAF-1 gene.  
270 <400> SEQUENCE: 6 35  
271 ggcatacgtc tagattagac gcagttatca gggac  
274 <210> SEQ ID NO: 7  
275 <211> LENGTH: 392  
276 <212> TYPE: PRT  
277 <213> ORGANISM: rat  
279 <400> SEQUENCE: 7  
281 Pro Thr Gly Thr Gly Cys Val Ile Leu Lys Ala Ser Ile Val Gln Lys  
282 1 5 10 15  
284 Arg Ile Ile Tyr Phe Gln Asp Glu Gly Ser Leu Thr Lys Lys Leu Cys  
285 20 25 30  
287 Glu Gln Asp Pro Thr Leu Asp Gly Val Thr Asp Arg Pro Ile Leu Asp  
288 35 40 45  
290 Cys.Cys Ala Cys Gly Thr Ala Lys Tyr Arg Leu Thr Phe Tyr Gly Asn  
291 50 55 60  
293 Trp Ser Glu Lys Thr His Pro Lys Asp Tyr Pro Arg Arg Ala Asn His  
294 65 70 75 80  
296 Trp Ser Ala Ile Ile Gly Gly Ser His Ser Lys Asn Tyr Val Leu Trp  
297 85 90 95  
299 Glu Tyr Gly Gly Tyr Ala Ser Glu Gly Val Lys Gln Val Ala Glu Leu  
300 100 105 110

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```

302 Gly Ser Pro Val Lys Met Glu Glu Glu Ile Arg Gln Gln Ser Asp Glu
303      115      120      125
305 Val Leu Thr Val Ile Lys Ala Lys Ala Gln Trp Pro Ser Trp Gln Pro
306      130      135      140
308 Val Asn Val Arg Ala Ala Pro Ser Ala Glu Phe Ser Val Asp Arg Thr
309 145      150      155      160
311 Arg His Leu Met Ser Phe Leu Thr Met Met Gly Pro Ser Pro Asp Trp
312      165      170      175
314 Asn Val Gly Leu Ser Ala Glu Asp Leu Cys Thr Lys Glu Cys Gly Trp
315      180      185      190
317 Val Gln Lys Val Val Gln Asp Leu Ile Pro Trp Asp Ala Gly Thr Asp
318      195      200      205
320 Ser Gly Val Thr Tyr Glu Ser Pro Asn Lys Pro Thr Ile Pro Gln Glu
321      210      215      220
323 Lys Ile Arg Pro Leu Thr Ser Leu Asp His Pro Gln Ser Pro Phe Tyr
324 225      230      235      240
326 Asp Pro Glu Gly Gly Ser Ile Thr Gln Val Ala Arg Val Val Ile Glu
327      245      250      255
329 Arg Ile Ala Arg Lys Gly Glu Gln Cys Asn Ile Val Pro Asp Asn Val
330      260      265      270
332 Asp Asp Ile Val Ala Asp Leu Ala Pro Glu Glu Lys Asp Glu Asp Asp
333      275      280      285
335 Thr Pro Glu Thr Cys Ile Tyr Ser Asn Trp Ser Pro Trp Ser Ala Cys
336      290      295      300
338 Ser Ser Ser Thr Cys Glu Lys Gly Lys Arg Met Arg Gln Arg Met Leu
339 305      310      315      320
341 Lys Ala Gln Leu Asp Leu Ser Val Pro Cys Pro Asp Thr Gln Asp Phe
342      325      330      335
344 Gln Pro Cys Met Gly Pro Gly Cys Ser Asp Glu Asp Gly Ser Thr Cys
345      340      345      350
347 Thr Met Ser Glu Trp Ile Thr Trp Ser Pro Cys Ser Val Ser Cys Gly
348      355      360      365
350 Met Gly Met Arg Ser Arg Glu Arg Tyr Val Lys Gln Phe Pro Glu Asp
351      370      375      380
353 Gly Ser Val Cys Met Leu Pro Thr
354 385      390
356 <210> SEQ ID NO: 8
357 <211> LENGTH: 52
358 <212> TYPE: PRT
359 <213> ORGANISM: rat
361 <400> SEQUENCE: 8
363 Cys Ile Tyr Ser Asn Trp Ser Pro Trp Ser Ala Cys Ser Ser Ser Thr
364 1      5      10      15
366 Cys Glu Lys Gly Lys Arg Met Arg Gln Arg Met Leu Lys Ala Gln Leu
367      20      25      30
369 Asp Leu Ser Val Pro Cys Pro Asp Thr Gln Asp Phe Gln Pro Cys Met
370      35      40      45
372 Gly Pro Gly Cys
373      50

```

*fyi*

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/170,042A

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Input Set : D:\PF226D1.txt

Output Set: N:\CRF3\03162001\I170042A.raw

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:495 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:  
L:677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:901 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:905 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:909 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18